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#21
Sub #25

SEQUENCE LISTING

<110> Brugliera, Filippa
Holton, Timothy A.
Michael, Michael Z.

<120> GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
AND USES THEREFOR

<130> 11658

<140> 09/142,108
<141> 1998-09-01

<150> PN8386
<151> 1996-03-01

<160> 45

<170> PatentIn Ver. 2.1

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<213> Petunia x hybrida

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Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His Leu Gly Pro
40 45 50

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Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Ala Ala Ser Ala
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Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn Phe Ser Ser
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Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp Phe Arg His					
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Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe Ala Asp Gly					
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Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser Met Val Val					
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His Pro Arg Pro Arg Leu Glu Ala Gln Ala Tyr Ile Gly				
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agtttggta tgctttggat ttagtagttt ttatattgat agatcaatgt ttgcattgtc				1708
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 Leu Pro Pro Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His
 35 40 45
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 Gly Pro Leu Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala
 65 70 75 80
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 85 90 95
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 100 105 110
 Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu
 115 120 125
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 130 135 140
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 Cys Thr Thr Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe
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 195 200 205
 Met Val Val Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp
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 Phe Ile Pro Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys
 225 230 235 240
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 245 250 255
 Glu Glu His Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser
 260 265 270
 Thr Leu Ile Ser Leu Lys Asn Asp Asp Ala Asp Asn Asp Gly Gly Lys
 275 280 285
 Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Val Ala
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Asn Leu Tyr Tyr Leu Ile Thr Thr Val Phe Arg Gly His Gln Lys Pro
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Leu Pro Pro Gly Pro Arg Pro Trp Pro Ile Val Gly Asn Leu Pro His
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Met Gly Gln Ala Pro His Gln Gly Leu Ala Ala Leu Ala Gln Lys Tyr
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Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Lys Trp Arg Met Leu
100 105 110
agg aaa att tgt tcc tta cac atg ttt tct tct aag gct ttg gac gat 561
Arg Lys Ile Cys Ser Leu His Met Phe Ser Ser Lys Ala Leu Asp Asp
115 120 125 130
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455	460	465	
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470	475	480	
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Lys Tyr Gly Pro Leu Leu Tyr Met Arg Leu Gly Tyr Val Asp Val Val			
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Val Ala Ala Ser Ala Ser Val Ala Thr Gln Phe Leu Lys Thr His Asp			
65 70 75 80			
Leu Asn Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His Ile Ala			
85 90 95			
Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Lys Trp Arg			
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115 120 125			
Asp Asp Phe Arg Leu Val Arg Gln Glu Glu Val Ser Ile Leu Val Asn			
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Ala Ile Ala Lys Ala Gly Thr Lys Pro Val Gln Leu Gly Gln Leu Leu			
145 150 155 160			
Asn Val Cys Thr Thr Asn Ala Leu Ser Arg Val Met Leu Gly Lys Arg			
165 170 175			
Val Leu Gly Asp Gly Thr Gly Lys Ser Asp Pro Lys Ala Glu Glu Phe			
180 185 190			

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 Gly Asp Phe Val Pro Ala Leu Glu Cys Leu Asp Leu Gln Gly Val Ala
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 Ser Lys Met Lys Lys Leu His Lys Arg Leu Asp Asn Phe Met Ser Asn
 225 230 235 240
 Ile Leu Glu Glu His Lys Ser Val Ala His Gln Gln Asn Gly Gly Asp
 245 250 255
 Leu Leu Ser Ile Leu Ile Ser Leu Lys Asp Asn Cys Asp Gly Glu Gly
 260 265 270
 Gly Lys Phe Ser Ala Thr Glu Ile Lys Ala Leu Leu Asp Leu Phe
 275 280 285
 Thr Ala Gly Thr Asp Thr Ser Ser Thr Thr Glu Trp Ala Ile Ala
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 305 310 315 320
 Asp Ser Val Val Gly Arg Asp Arg Leu Ile Ala Glu Ala Asp Ile Pro
 325 330 335
 Asn Leu Thr Tyr Phe Gln Ala Val Ile Lys Glu Val Phe Arg Leu His
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 Pro Ser Thr Pro Leu Ser Leu Pro Arg Val Ala Asn Glu Ser Cys Glu
 355 360 365
 Ile Asn Gly Tyr His Ile Pro Lys Asn Thr Thr Leu Leu Val Asn Val
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 Trp Ala Ile Ala Arg Asp Pro Glu Val Trp Ala Asp Pro Leu Glu Phe
 385 390 395 400
 Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val Asp Val
 405 410 415
 Lys Gly Asn Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile
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 Cys Ala Gly Leu Ser Leu Gly Leu Arg Met Val Gln Leu Met Thr Ala
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 Thr Leu Ala His Thr Tyr Asp Trp Ala Leu Ala Asp Gly Leu Met Pro
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 Glu Lys Leu Asn Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln Arg Lys
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Val Leu Ala Asp Ala Gly Glu Thr Pro Leu Lys Leu Gly Gln Met Met			
170	175	180	
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205	210	215	
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Val Glu Leu Met Val Leu Ala Gly Val Phe Asn Leu Gly Asp Phe Ile			
220	225	230	
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Pro Pro Leu Glu Lys Leu Asp Leu Gln Gly Val Ile Ala Lys Met Lys			
235	240	245	
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Lys Leu His Leu Arg Phe Asp Ser Phe Leu Ser Lys Ile Leu Gly Asp			
250	255	260	
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His	Lys	Ile	Asn	Ser	Ser	Asp	Glu	Thr	Lys	Gly	His	Ser	Asp	Leu	Leu		
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Asn	Met	Leu	Ile	Ser	Leu	Lys	Asp	Ala	Asp	Asp	Ala	Glu	Gly	Gly	Arg		
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ctc	acc	gac	gta	gaa	att	aaa	gcg	ttg	ctc	ttg	aac	ttg	ttt	gct	gca	1026	
Leu	Thr	Asp	Val	Glu	Ile	Lys	Ala	Leu	Leu	Leu	Asn	Leu	Phe	Ala	Ala		
					300				305				310				
gga	act	gac	aca	aca	tca	agc	act	gtg	gaa	tgg	tgc	ata	gct	gag	tta	1074	
Gly	Thr	Asp	Thr	Thr	Ser	Ser	Thr	Val	Glu	Trp	Cys	Ile	Ala	Glu	Leu		
					315				320			325					
gta	cga	cat	cct	gaa	atc	ctt	gcc	caa	gtc	caa	aaa	gaa	ctc	gac	tct	1122	
Val	Arg	His	Pro	Glu	Ile	Leu	Ala	Gln	Val	Gln	Lys	Glu	Leu	Asp	Ser		
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gtt	gtt	gtt	aag	aat	cgg	gtg	gtg	aag	gag	gct	gat	ctg	gcc	gga	tta	1170	
Val	Val	Gly	Lys	Asn	Arg	Val	Val	Lys	Glu	Ala	Asp	Leu	Ala	Gly	Leu		
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cca	ttc	ctc	caa	gcg	gtc	gtc	aag	gaa	aat	ttc	cga	ctc	cat	ccc	tcc	1218	
Pro	Phe	Leu	Gln	Ala	Val	Val	Lys	Glu	Asn	Phe	Arg	Leu	His	Pro	Ser		
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acc	ccg	ctc	tcc	cta	ccg	agg	atc	gca	cat	gag	agt	tgt	gaa	gtg	aat	1266	
Thr	Pro	Leu	Ser	Leu	Pro	Arg	Ile	Ala	His	Glu	Ser	Cys	Glu	Val	Asn		
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Gly	Tyr	Leu	Ile	Pro	Lys	Gly	Ser	Thr	Leu	Leu	Val	Asn	Val	Trp	Ala		
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att	gct	cgc	gat	cca	aat	gtg	tgg	gat	gaa	cca	cta	gag	ttc	cgg	cct	1362	
Ile	Ala	Arg	Asp	Pro	Asn	Val	Trp	Asp	Glu	Pro	Leu	Glu	Phe	Arg	Pro		
					410				415			420					
gaa	cga	ttc	ttg	aag	ggc	ggg	gaa	aag	cct	aat	gtc	gat	gtt	aga	ggg	1410	
Glu	Arg	Phe	Leu	Lys	Gly	Gly	Glu	Lys	Pro	Asn	Val	Asp	Val	Arg	Gly		
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aat	gat	ttc	gaa	ttg	ata	ccg	ttc	gga	gcf	ggc	cga	aga	att	tgt	gca	1458	
Asn	Asp	Phe	Glu	Leu	Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala		
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Gly	Met	Ser	Leu	Gly	Ile	Arg	Met	Val	Gln	Leu	Leu	Thr	Ala	Thr	Leu		
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aac	cat	gcf	ttt	gac	ttt	gat	ttg	gcf	gat	gga	cag	ttg	cct	gaa	agc	1554	
Asn	His	Ala	Phe	Asp	Phe	Asp	Leu	Ala	Asp	Gly	Gln	Leu	Pro	Glu	Ser		
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tta	aac	atg	gag	gaa	gct	tat	ggg	ctg	acc	ttg	caa	cga	gct	gac	cct	1602	
Leu	Asn	Met	Glu	Glu	Ala	Tyr	Gly	Leu	Thr	Leu	Gln	Arg	Ala	Asp	Pro		
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ttg	gta	gtg	cac	ccg	aag	cct	agg	tag	gcacctatg	tttatcaaac						1649	
Leu	Val	Val	His	Pro	Lys	Pro	Arg										
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1711

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Tyr Ser Phe Leu Asn Lys Lys Val Lys Pro Leu Pro Pro Gly Pro Lys
35 40 45
Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu Gly Pro Lys Pro His
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Gln Ser Met Ala Ala Leu Ala Arg Val His Gly Pro Leu Ile His Leu
65 70 75 80
Lys Met Gly Phe Val His Val Val Ala Ser Ser Ala Ser Val Ala
85 90 95
Glu Lys Phe Leu Lys Val His Asp Ala Asn Phe Ser Ser Arg Pro Pro
100 105 110
Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr Gln Asp Leu Val Phe
115 120 125
Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu Arg Lys Ile Cys Ala Leu
130 135 140
His Leu Phe Ser Ala Lys Ala Leu Asn Asp Phe Thr His Val Arg Gln
145 150 155 160
Asp Glu Val Gly Ile Leu Thr Arg Val Leu Ala Asp Ala Gly Glu Thr
165 170 175
Pro Leu Lys Leu Gly Gln Met Met Asn Thr Cys Ala Thr Asn Ala Ile
180 185 190
Ala Arg Val Met Leu Gly Arg Arg Val Val Gly His Ala Asp Ser Lys
195 200 205
Ala Glu Glu Phe Lys Ala Met Val Val Glu Leu Met Val Leu Ala Gly
210 215 220
Val Phe Asn Leu Gly Asp Phe Ile Pro Pro Leu Glu Lys Leu Asp Leu
225 230 235 240
Gln Gly Val Ile Ala Lys Met Lys Lys Leu His Leu Arg Phe Asp Ser
245 250 255
Phe Leu Ser Lys Ile Leu Gly Asp His Lys Ile Asn Ser Ser Asp Glu
260 265 270
Thr Lys Gly His Ser Asp Leu Leu Asn Met Leu Ile Ser Leu Lys Asp
275 280 285
Ala Asp Asp Ala Glu Gly Gly Arg Leu Thr Asp Val Glu Ile Lys Ala
290 295 300
Leu Leu Leu Asn Leu Phe Ala Ala Gly Thr Asp Thr Thr Ser Ser Thr
305 310 315 320
Val Glu Trp Cys Ile Ala Glu Leu Val Arg His Pro Glu Ile Leu Ala
325 330 335
Gln Val Gln Lys Glu Leu Asp Ser Val Val Gly Lys Asn Arg Val Val
340 345 350
Lys Glu Ala Asp Leu Ala Gly Leu Pro Phe Leu Gln Ala Val Val Lys
355 360 365
Glu Asn Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu Pro Arg Ile
370 375 380
Ala His Glu Ser Cys Glu Val Asn Gly Tyr Leu Ile Pro Lys Gly Ser
385 390 395 400

Thr	Leu	Leu	Val	Asn	Val	Trp	Ala	Ile	Ala	Arg	Asp	Pro	Asn	Val	Trp
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Asp	Glu	Pro	Leu	Glu	Phe	Arg	Pro	Glu	Arg	Phe	Leu	Lys	Gly	Gly	Glu
				420				425				430			
Lys	Pro	Asn	Val	Asp	Val	Arg	Gly	Asn	Asp	Phe	Glu	Leu	Ile	Pro	Phe
				435			440				445				
Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Met	Ser	Leu	Gly	Ile	Arg	Met
				450			455			460					
Val	Gln	Leu	Leu	Thr	Ala	Thr	Leu	Asn	His	Ala	Phe	Asp	Phe	Asp	Leu
				465			470			475					480
Ala	Asp	Gly	Gln	Leu	Pro	Glu	Ser	Leu	Asn	Met	Glu	Glu	Ala	Tyr	Gly
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Asp	Gly	Gly	Ser	Leu	Thr	Asp	Thr	Glu	Ile	Lys	Ala	Leu	Leu	Asn		
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atg	ttc	aca	gct	gga	act	gac	acg	tca	gca	agt	acg	gtg	gac	tgg	gct	144
Met	Phe	Thr	Ala	Gly	Thr	Asp	Thr	Ser	Ala	Ser	Thr	Val	Asp	Trp	Ala	
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ata	gct	gaa	ctt	atc	cgt	cac	ccg	gat	ata	atg	gtt	aaa	gcc	caa	gaa	192
Ile	Ala	Glu	Leu	Ile	Arg	His	Pro	Asp	Ile	Met	Val	Lys	Ala	Gln	Glu	
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gaa	ctt	gat	att	gtt	gtg	ggc	cgt	gac	agg	cct	gtt	aat	gaa	tca	gac	240
Glu	Leu	Asp	Ile	Val	Val	Gly	Arg	Asp	Arg	Pro	Val	Asn	Glu	Ser	Asp	
						65			70			75			80	
atc	gct	cag	ctt	cct	tac	ctt	cag	gcg	gtt	atc	aaa	gag	aat	ttc	agg	288
Ile	Ala	Gln	Leu	Pro	Tyr	Leu	Gln	Ala	Val	Ile	Lys	Glu	Asn	Phe	Arg	
								85		90					95	
ctt	cat	cca	cca	aca	cca	ctc	tcg	tta	cca	cac	atc	gcg	tca	gag	agc	336
Leu	His	Pro	Pro	Thr	Pro	Leu	Ser	Leu	Pro	His	Ile	Ala	Ser	Glu	Ser	
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tgt	gag	atc	aac	ggc	tac	cat	atc	ccg	aaa	gga	tcg	act	cta	ttt	gac	384
Cys	Glu	Ile	Asn	Gly	Tyr	His	Ile	Pro	Lys	Gly	Ser	Thr	Leu	Phe	Asp	
								115		120					125	
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Gly	His	Met	Gly	Leu	Gly	Arg	Asp	Pro	Asp	Gln	Trp	Ser	Asp	Pro	Leu	
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Asp Val Lys Gly Ser Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg		
165	170	175
cca atc tgt gca ggt tta agt tta ggg cta cgt aca gat tta agt tgc		576
Pro Ile Cys Ala Gly Leu Ser Leu Gly Leu Arg Thr Asp Leu Ser Cys		
180	185	190
ctt cac gcc aac gtt gct cac aag cat ttg att ggg aac ttc agc tgg		624
Leu His Ala Asn Val Ala His Lys His Leu Ile Gly Asn Phe Ser Trp		
195	200	205
aga agt tac gcc gga caa cct gaa tat cgc agg aaa agt tta ctg ggc		672
Arg Ser Tyr Ala Gly Gln Pro Glu Tyr Arg Arg Lys Ser Leu Leu Gly		
210	215	220
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Phe Thr Leu Gln Arg Ala Val Pro Ser Val Val His Pro Lys Pro Arg		
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240		
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Leu Ala Pro Asn Val Tyr Gly Pro Arg Val Gly Leu Lys Phe Asn Phe		
245	250	255
gct tct tgg aca agg tat atg gct tgc acg aaa cta acg ttt taa		813
Ala Ser Trp Thr Arg Tyr Met Ala Cys Thr Lys Leu Thr Phe		
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35 40 45
Ile Ala Glu Leu Ile Arg His Pro Asp Ile Met Val Lys Ala Gln Glu
50 55 60
Glu Leu Asp Ile Val Val Gly Arg Asp Arg Pro Val Asn Glu Ser Asp
65 70 75 80
Ile Ala Gln Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Asn Phe Arg
85 90 95
Leu His Pro Pro Thr Pro Leu Ser Leu Pro His Ile Ala Ser Glu Ser
100 105 110
Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Phe Asp
115 120 125

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Pro	Ile	Cys	Ala	Gly	Leu	Ser	Leu	Gly	Leu	Arg	Thr	Asp	Leu	Ser	Cys
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					210			215			220				
Phe	Thr	Leu	Gln	Arg	Ala	Val	Pro	Ser	Val	Val	His	Pro	Lys	Pro	Arg
225					230				235			240			
Leu	Ala	Pro	Asn	Val	Tyr	Gly	Pro	Arg	Val	Gly	Leu	Lys	Phe	Asn	Phe
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His Leu Phe Ser Ala Lys Ala Leu Glu Asp Phe Lys His Val Arg Gln			
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Glu Glu Val Gly Thr Leu Thr Arg Glu Leu Val Arg Val Gly Thr			
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Lys Pro Val Asn Leu Gly Gln Leu Val Asn Met Cys Val Val Asn Ala			
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cta gga cga gag atg atc gga cgg cga ctg ttc ggc gcc gac gcc gat			2791
Leu Gly Arg Glu Met Ile Gly Arg Arg Leu Phe Gly Ala Asp Ala Asp			
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His Lys Ala Asp Glu Phe Arg Ser Met Val Thr Glu Met Met Ala Leu			
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gcc gga gta ttt aac atc gga gat ttc gtg ccg tca ctt gat tgg tta			2887
Ala Gly Val Phe Asn Ile Gly Asp Phe Val Pro Ser Leu Asp Trp Leu			
65 70 75			
gat tta caa ggc gtc gct ggt aaa atg aaa cgg ctt cac aaa aga ttc			2935
Asp Leu Gln Gly Val Ala Gly Lys Met Lys Arg Leu His Lys Arg Phe			
80 85 90 95			
gac gct ttt cta tcg tcg att ttg aaa gag cac gaa atg aac ggt caa			2983
Asp Ala Phe Leu Ser Ser Ile Leu Lys Glu His Glu Met Asn Gly Gln			
100 105 110			
gat caa aag cat aca gat atg ctt agc act tta atc tcc ctt aaa gga			3031
Asp Gln Lys His Thr Asp Met Leu Ser Thr Leu Ile Ser Leu Lys Gly			
115 120 125			

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cta ttg acg aac ata tgg gcc ata gcc cgt gac ccg gat caa tgg tcc Leu Leu Thr Asn Ile Trp Ala Ile Ala Arg Asp Pro Asp Gln Trp Ser 40 45 50	3579
gac ccg tta gca ttt aaa ccc gag aga ttc tta ccc ggt ggt gaa aaa Asp Pro Leu Ala Phe Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys 55 60 65	3627
tcc ggc gtt gat gtg aaa gga agc gat ttc gag cta ata ccg ttc gga Ser Gly Val Asp Val Lys Gly Ser Asp Phe Glu Leu Ile Pro Phe Gly 70 75 80 85	3675
gct ggg agg aga atc tgt gcc ggt tta agt tta ggg tta cgt acg att Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Leu Gly Leu Arg Thr Ile 90 95 100	3723
cag ttt ctt acg gcg acg ttg gtt caa gga ttt gat tgg gaa tta gct Gln Phe Leu Thr Ala Thr Leu Val Gln Gly Phe Asp Trp Glu Leu Ala 105 110 115	3771
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Thr Leu Gln Arg Ala Val Pro Leu Val Val His Pro Lys Pro Arg Leu	
135 140 145	
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Ala Pro Asn Val Tyr Gly Leu Gly Ser Gly	
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20	25	30	
Leu Pro Pro Gly Pro Asn Pro Trp Pro Ile Ile Gly Asn Leu Pro His			
35	40	45	
Met Gly Thr Lys Pro His Arg Thr Leu Ser Ala Met Val Thr Thr Tyr			
50	55	60	
Gly Pro Ile Leu His Leu Arg Leu Gly Phe Val Asp Val Val Val Ala			
65	70	75	80
Ala Ser Lys Ser Val Ala Glu Gln Phe Leu Lys Ile His Asp Ala Asn			
85	90	95	
Phe Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Met Ala Tyr Asn			
100	105	110	

Tyr	Gln	Asp	Leu	Val	Phe	Ala	Pro	Tyr	Gly	His	Arg	Trp	Arg	Leu	Leu
115								120				125			
Arg	Lys	Ile	Ser	Ser	Val	His	Leu	Phe	Ser	Ala	Lys	Ala	Leu	Glu	Asp
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Phe	Lys	His	Val	Arg	Gln										
145					150										

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Pro	Val	Asn	Leu	Gly	Gln	Leu	Val	Asn	Met	Cys	Val	Val	Asn	Ala	Leu
			20					25					30		

Gly	Arg	Glu	Met	Ile	Gly	Arg	Arg	Leu	Phe	Gly	Ala	Asp	Ala	Asp	His
			35				40					45			

Lys	Ala	Asp	Glu	Phe	Arg	Ser	Met	Val	Thr	Glu	Met	Met	Ala	Leu	Ala
			50				55				60				

Gly	Val	Phe	Asn	Ile	Gly	Asp	Phe	Val	Pro	Ser	Leu	Asp	Trp	Leu	Asp
			65				70			75			80		

Leu	Gln	Gly	Val	Ala	Gly	Lys	Met	Lys	Arg	Leu	His	Lys	Arg	Phe	Asp
							85			90			95		

Ala	Phe	Leu	Ser	Ser	Ile	Leu	Lys	Glu	His	Glu	Met	Asn	Gly	Gln	Asp
								105			110				

Gln	Lys	His	Thr	Asp	Met	Leu	Ser	Thr	Leu	Ile	Ser	Leu	Lys	Gly	Thr
			115				120					125			

Asp	Leu	Asp	Gly	Asp	Gly	Gly	Ser	Leu	Thr	Asp	Thr	Glu	Ile	Lys	Ala
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Leu	Leu	Leu													
145															

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<400> 12															
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Ala	Ile	Ala	Glu	Leu	Ile	Arg	His	Pro	Asp	Ile	Met	Val	Lys	Ala	Gln
								20			25		30		

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35 40 45

Asp Ile Ala Gln Leu Pro Tyr Leu Gln
50 55

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<212> PRT
<213> Arabidopsis thaliana

<400> 13
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20 25 30

Pro Lys Gly Ser Thr Leu Leu Thr Asn Ile Trp Ala Ile Ala Arg Asp
35 40 45

Pro Asp Gln Trp Ser Asp Pro Leu Ala Phe Lys Pro Glu Arg Phe Leu
50 55 60

Pro Gly Gly Glu Lys Ser Gly Val Asp Val Lys Gly Ser Asp Phe Glu
65 70 75 80

Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Leu
85 90 95

Gly Leu Arg Thr Ile Gln Phe Leu Thr Ala Thr Leu Val Gln Gly Phe
100 105 110

Asp Trp Glu Leu Ala Gly Val Thr Pro Glu Lys Leu Asn Met Glu
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Glu Ser Tyr Gly Leu Thr Leu Gln Arg Ala Val Pro Leu Val Val His
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Pro Lys Pro Arg Leu Ala Pro Asn Val Tyr Gly Leu Gly Ser Gly
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tcc gcc gtg ttt ttg ttc cgg ctt ctt ttc tcc ggc aaa tcc caa cgc 99
Phe Ala Val Phe Leu Phe Arg Leu Leu Phe Ser Gly Lys Ser Gln Arg
15 20 25

cac tcg ctc cct ctc cct ggc ccc aaa cca tgg ccg gtg gtt ggc		147	
His Ser Leu Pro Leu Pro Pro Gly Pro Lys Pro Trp Pro Val Val Gly			
30	35	40	
aac tta cct cac ttg ggc ccc ttc ccg cac cac tcc atc gcg gag ttg		195	
Asn Leu Pro His Leu Gly Pro Phe Pro His His Ser Ile Ala Glu Leu			
45	50	55	
gcg aag aaa cac ggg ccg ctc atg cac ctc cgc ctc ggc tac gtt gac		243	
Ala Lys Lys His Gly Pro Leu Met His Leu Arg Leu Gly Tyr Val Asp			
60	65	70	
gta gtc gtg gcg gca tca gca tcc gta gcg gcc cag ttc ttg aag act		291	
Val Val Val Ala Ala Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Thr			
75	80	85	90
cac gac gcc aat ttc tcc agc cga ccg ccc aac tcc ggc gcc aag cac		339	
His Asp Ala Asn Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Lys His			
95	100	105	
ctc gcc tat aac tac cag gac ctc gtg ttc agg ccg tac ggt cca cgg		387	
Leu Ala Tyr Asn Tyr Gln Asp Leu Val Phe Arg Pro Tyr Gly Pro Arg			
110	115	120	
tgg cgc atg ttc cg ^g aag atc agc tcc gtc cat ctg ttc tcc ggc aaa		435	
Trp Arg Met Phe Arg Lys Ile Ser Ser Val His Leu Phe Ser Gly Lys			
125	130	135	
gcc ttg gat gat ctt aaa cac gtc cg ^g cag gag gag gta agt gtg cta		483	
Ala Leu Asp Asp Leu Lys His Val Arg Gln Glu Val Ser Val Leu			
140	145	150	
g ^c cat gcc ttg gca aat tca ggg tca aag gta gtg aac ctg g ^c caa		531	
Ala His Ala Leu Ala Asn Ser Gly Ser Lys Val Val Asn Leu Ala Gln			
155	160	165	170
ctg ctg aac ctg tgc acg gtc aat gct cta gga agg gtg atg gta ggg		579	
Leu Leu Asn Leu Cys Thr Val Asn Ala Leu Gly Arg Val Met Val Gly			
175	180	185	
cgg agg gtt ttc ggc gac ggc agc gga ggc gac gat ccg aag g ^c gac		627	
Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Asp Asp Pro Lys Ala Asp			
190	195	200	
gag ttc aaa tcg atg gtg gtg gag atg atg gtg ttg gca gga gtg ttc		675	
Glu Phe Lys Ser Met Val Val Glu Met Met Val Leu Ala Gly Val Phe			
205	210	215	
aac ata ggt gac ttc atc ccc tct ctc gaa tgg ctt gac ttg caa ggc		723	
Asn Ile Gly Asp Phe Ile Pro Ser Leu Glu Trp Leu Asp Leu Gln Gly			
220	225	230	
gtg g ^c tcc aag atg aag aag ctc cac aag aga ttc gac gac ttc ttg		771	
Val Ala Ser Lys Met Lys Lys Leu His Lys Arg Phe Asp Asp Phe Leu			
235	240	245	250
aca gcc att gtc gag gac cac aag aag ggc tcc ggc acg g ^c ggg cac		819	
Thr Ala Ile Val Glu Asp His Lys Lys Ser Gly Ser Gly Thr Ala Gly His			
255	260	265	
gtc gac atg ttg acc act ctg ctc tcg ctc aag gaa gac gcc gac ggc		867	
Val Asp Met Leu Thr Thr Leu Leu Ser Leu Lys Glu Asp Ala Asp Gly			
270	275	280	

gaa gga ggc aag ctc acc gat act gaa atc aaa gct ttg ctt ttg aac	915
Glu Gly Lys Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn	
285	290
295	
atg ttc acg gct ggc act gat acg tca tcg agc acg gtg gaa tgg gca	963
Met Phe Thr Ala Gly Thr Asp Thr Ser Ser Ser Thr Val Glu Trp Ala	
300	305
310	
ata gct gaa ctc att cgg cac cct cat atg cta gcg cga gtt cag aaa	1011
Ile Ala Glu Leu Ile Arg His Pro His Met Leu Ala Arg Val Gln Lys	
315	320
325	330
gag ctt gac gat ttt gtt ggc cat gac cga ctt gtg acc gaa tcc gac	1059
Glu Leu Asp Asp Phe Val Gly His Asp Arg Leu Val Thr Glu Ser Asp	
335	340
345	
ata ccc aac ctc cct tac ctc caa gcc gtg atc aag gaa acg ttc cga	1107
Ile Pro Asn Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Thr Phe Arg	
350	355
360	
ctc cac cca tcc act cct ctc tcg ttg cct cgt atg gca gcc gag agt	1155
Leu His Pro Ser Thr Pro Leu Ser Leu Pro Arg Met Ala Ala Glu Ser	
365	370
375	
tgc gaa atc aac ggg tac cac atc ccg aaa ggc tcc aca ctc ttg gtc	1203
Cys Glu Ile Asn Gly Tyr His Ile Pro Lys Gly Ser Thr Leu Leu Val	
380	385
390	
aat gta tgg gcc ata tcg cgt gac ccg gct gaa tgg gcc gac cca ctg	1251
Asn Val Trp Ala Ile Ser Arg Asp Pro Ala Glu Trp Ala Asp Pro Leu	
395	400
405	410
gag ttc aag ccc gag agg ttc ctg ccg ggg ggc gaa aag cct aat gtt	1299
Glu Phe Lys Pro Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val	
415	420
425	
gat att aga gga aac gat ttt gaa gtc ata ccc ttc ggt gcc ggg cga	1347
Asp Ile Arg Gly Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg	
430	435
440	
aga ata tgt gcc ggg atg agc ttg ggc ctg cgt atg gtc cat tta atg	1395
Arg Ile Cys Ala Gly Met Ser Leu Gly Leu Arg Met Val His Leu Met	
445	450
455	
act gca aca ttg gtc cac gca ttt aat tgg gcc ttg gct gat ggg ctg	1443
Thr Ala Thr Leu Val His Ala Phe Asn Trp Ala Leu Ala Asp Gly Leu	
460	465
470	
acc gct gag aag tta aac atg gat gaa gca tat ggg ctc act cta caa	1491
Thr Ala Glu Lys Leu Asn Met Asp Glu Ala Tyr Gly Leu Thr Leu Gln	
475	480
485	490
cga gct gca ccg tta atg gtg cac ccg cgc acc agg ctg gcc cca cag	1539
Arg Ala Ala Pro Leu Met Val His Pro Arg Thr Arg Leu Ala Pro Gln	
495	500
505	
gca tat aaa act tca tca tct taa tttagagagct atgttctggg tgtccccgt	1593

Ala Tyr Lys Thr Ser Ser Ser	
510	
ttgatgtctc catgtttctt attttaggttt aaatctgtaa gataaggta ttctatgctg	1653
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Pro Gly Pro Lys Pro Trp Pro Val Val Gly Asn Leu Pro His Leu Gly
35 40 45
Pro Phe Pro His His Ser Ile Ala Glu Leu Ala Lys Lys His Gly Pro
50 55 60
Leu Met His Leu Arg Leu Gly Tyr Val Asp Val Val Val Ala Ala Ser
65 70 75 80
Ala Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn Phe Ser
85 90 95
Ser Arg Pro Pro Asn Ser Gly Ala Lys His Leu Ala Tyr Asn Tyr Gln
100 105 110
Asp Leu Val Phe Arg Pro Tyr Gly Pro Arg Trp Arg Met Phe Arg Lys
115 120 125
Ile Ser Ser Val His Leu Phe Ser Gly Lys Ala Leu Asp Asp Leu Lys
130 135 140
His Val Arg Gln Glu Glu Val Ser Val Leu Ala His Ala Leu Ala Asn
145 150 155 160
Ser Gly Ser Lys Val Val Asn Leu Ala Gln Leu Leu Asn Leu Cys Thr
165 170 175
Val Asn Ala Leu Gly Arg Val Met Val Gly Arg Arg Val Phe Gly Asp
180 185 190
Gly Ser Gly Gly Asp Asp Pro Lys Ala Asp Glu Phe Lys Ser Met Val
195 200 205
Val Glu Met Met Val Leu Ala Gly Val Phe Asn Ile Gly Asp Phe Ile
210 215 220
Pro Ser Leu Glu Trp Leu Asp Leu Gln Gly Val Ala Ser Lys Met Lys
225 230 235 240
Lys Leu His Lys Arg Phe Asp Asp Phe Leu Thr Ala Ile Val Glu Asp
245 250 255
His Lys Lys Gly Ser Gly Thr Ala Gly His Val Asp Met Leu Thr Thr
260 265 270
Leu Leu Ser Leu Lys Glu Asp Ala Asp Gly Glu Gly Lys Leu Thr
275 280 285
Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Met Phe Thr Ala Gly Thr
290 295 300
Asp Thr Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg
305 310 315 320
His Pro His Met Leu Ala Arg Val Gln Lys Glu Leu Asp Asp Phe Val
325 330 335
Gly His Asp Arg Leu Val Thr Glu Ser Asp Ile Pro Asn Leu Pro Tyr
340 345 350
Leu Gln Ala Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro
355 360 365
Leu Ser Leu Pro Arg Met Ala Ala Glu Ser Cys Glu Ile Asn Gly Tyr
370 375 380
His Ile Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ser
385 390 395 400
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<213> Chrysanthemum

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<222> (4)..(1530)

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gta ctc tat gta ttt ctt aac tta agt tca cgt aaa tcc gcc aga ctc	96	
Val Leu Tyr Val Phe Leu Asn Leu Ser Ser Arg Lys Ser Ala Arg Leu		
20	25	30

cca ccc ggg cca aca cca tgg cct ata gtc ggg aac tta cca cac ctt 144
 Pro Pro Gly Pro Thr Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu
 35 40 45

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ggc cca atc cca cac cac gca ctc gcg gcc tta gcc aag aag tac ggg 192
Gly Pro Ile Pro His His Ala Leu Ala Ala Leu Ala Lys Lys Tyr Gly
      50           55           60

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tct gct tcc gta gct gca cag ttt tta aaa gtt cac gac gca aat ttt 288
Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Val His Asp Ala Asn Phe
 80          85          90          95
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gct agt agg ccg cca aat tct ggc gcg aaa cat gtg gcg tat aat tat 336
Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr
          100          105          110

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cag gat ctt gtg ttt gca cct tat ggt cca agg tgg cgt ttg tta agg 384
Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Leu Leu Arg
          115           120           125

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aag att tgt tcg gtc cat ttg ttt tct gct aaa gca ctt gat gat ttt	432		
Lys Ile Cys Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe			
130	135	140	

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cgt cat gtt cga cag gag gag gta gca gtc cta acc cgc gta cta ctg 480
Arg His Val Arg Gln Glu Glu Val Ala Val Leu Thr Arg Val Leu Leu
          145           150           155

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agt gct gga aac tca ccg gta cag ctt ggc caa cta ctt aac gtg tgt	528
Ser Ala Gly Asn Ser Pro Val Gln Leu Gly Gln Leu Leu Asn Val Cys	
160 165 170 175	
gcc aca aac gcc tta gca cg ^g gta atg tta ggt agg aga gtt ttc gga	576
Ala Thr Asn Ala Leu Ala Arg Val Met Leu Gly Arg Arg Val Phe Gly	
180 185 190	
gac gga att gac agg tca gcc aat gag ttc aaa gat atg gta gta gag	624
Asp Gly Ile Asp Arg Ser Ala Asn Glu Phe Lys Asp Met Val Val Glu	
195 200 205	
tta atg gta tta gca gga gaa ttt aac ctt ggt gac ttt att cct gta	672
Leu Met Val Leu Ala Gly Glu Phe Asn Leu Gly Asp Phe Ile Pro Val	
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Leu Asp Leu Phe Asp Leu Gln Gly Ile Thr Lys Lys Met Lys Lys Leu	
225 230 235	
cat gtt cg ^g ttc gat tca ttt ctt agt aag atc gtt gag gag cat aaa	768
His Val Arg Phe Asp Ser Phe Leu Ser Lys Ile Val Glu Glu His Lys	
240 245 250 255	
acg gca cct ggt ggg ttg ggt cat act gat ttg ctg agc acg ttg att	816
Thr Ala Pro Gly Gly Leu Gly His Thr Asp Leu Leu Ser Thr Leu Ile	
260 265 270	
tca ctt aaa gat gat gct gat att gaa ggt ggg aag ctt aca gat act	864
Ser Leu Lys Asp Asp Ala Asp Ile Glu Gly Gly Lys Leu Thr Asp Thr	
275 280 285	
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Glu Ile Lys Ala Leu Leu Asn Leu Phe Ala Ala Gly Thr Asp Thr	
290 295 300	
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Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg His Pro	
305 310 315	
caa ata tta aaa caa gcc cga gaa gag ata gac gct gta gtt ggt caa	1008
Gln Ile Leu Lys Gln Ala Arg Glu Glu Ile Asp Ala Val Val Gly Gln	
320 325 330 335	
gac cg ^g ctt gta aca gaa ttg gac ttg agc caa cta aca tac ctc cag	1056
Asp Arg Leu Val Thr Glu Leu Asp Leu Ser Gln Leu Thr Tyr Leu Gln	
340 345 350	
gct ctt gtg aaa gag gtg ttt agg ctc cac cct tca acg cca ctc tcc	1104
Ala Leu Val Lys Glu Val Phe Arg Leu His Pro Ser Thr Pro Leu Ser	
355 360 365	
tta cca aga ata tca tcc gag agt tgt gag gtc gat ggg tat tat atc	1152
Leu Pro Arg Ile Ser Ser Glu Ser Cys Glu Val Asp Gly Tyr Tyr Ile	
370 375 380	
cct aag gga tcc aca ctc ctc gtt aac gtg tgg gcc att gc ^g cga gac	1200
Pro Lys-Gly-Ser-Thr-Leu-Leu-Val-Asn-Val-Trp-Ala-Ile-Ala-Arg-Asp	
385 390 395	
cca aaa atg tgg gc ^g gat cct ctt gaa ttt agg cct tct cgg ttt tta	1248
Pro Lys Met Trp Ala Asp Pro Leu Glu Phe Arg Pro Ser Arg Phe Leu	
400 405 410 415	

ccc ggg gga gaa aag ccc ggt gct gat gtt agg gga aat gat ttt gaa	1296
Pro Gly Gly Glu Lys Pro Gly Ala Asp Val Arg Gly Asn Asp Phe Glu	
420	425
	430
gtt ata cca ttt ggg gca gga cga agg att tgt gcg ggt atg agc cta	1344
Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu	
435	440
	445
ggc ttg aga atg gtc cag ttg ctc att gca aca ttg gtc caa act ttt	1392
Gly Leu Arg Met Val Gln Leu Ile Ala Thr Leu Val Gln Thr Phe	
450	455
	460
gat tgg gaa ctg gct aac ggg tta gag ccg gag atg ctc aac atg gaa	1440
Asp Trp Glu Leu Ala Asn Gly Leu Pro Glu Met Leu Asn Met Glu	
465	470
	475
gaa gcg tat gga ttg acc ctt caa cgg gct gca ccc ttg atg gtt cac	1488
Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met Val His	
480	485
	490
	495
ccg aag ccg agg tta gct ccc cac gta tat gaa agt att taa	1530
Pro Lys Pro Arg Leu Ala Pro His Val Tyr Glu Ser Ile	
500	505
ggactagttt ctctttgcc tttttgttc gcaaaggta atgaataaac gattcatga	1590
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aaaaaaaaaa	1660
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Pro Gly Pro Thr Pro Trp Pro Ile Val Gly Asn Leu Pro His Leu Gly	
35 40 45	
Pro Ile Pro His His Ala Leu Ala Ala Leu Ala Lys Lys Tyr Gly Pro	
50 55 60	
Leu Met His Leu Arg Leu Gly Cys Val Asp Val Val Val Ala Ala Ser	
65 70 75 80	
Ala Ser Val Ala Ala Gln Phe Leu Lys Val His Asp Ala Asn Phe Ala	
85 90 95	
Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr Asn Tyr Gln	
100 105 110	
Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys	
115 120 125	
Ile Cys Ser Val His Leu Phe Ser Ala Lys Ala Leu Asp Asp Phe Arg	
130 135 140	
His Val Arg Gln Glu Glu Val Ala Val Leu Thr Arg Val Leu Leu Ser	
145 150 155 160	
Ala Gly Asn Ser Pro Val Gln Leu Gly Gln Leu Leu Asn Val Cys Ala	
165 170 175	
Thr Asn Ala Leu Ala Arg Val Met Leu Gly Arg Arg Val Phe Gly Asp	
180 185 190	
Gly Ile Asp Arg Ser Ala Asn Glu Phe Lys Asp Met Val Val Glu Leu	
195 200 205	

Met	Val	Leu	Ala	Gly	Glu	Phe	Asn	Leu	Gly	Asp	Phe	Ile	Pro	Val	Leu
210				215					220						
Asp	Leu	Phe	Asp	Leu	Gln	Gly	Ile	Thr	Lys	Lys	Met	Lys	Lys	Leu	His
225				230					235						240
Val	Arg	Phe	Asp	Ser	Phe	Leu	Ser	Lys	Ile	Val	Glu	Glu	His	Lys	Thr
				245				250						255	
Ala	Pro	Gly	Gly	Leu	Gly	His	Thr	Asp	Leu	Leu	Ser	Thr	Leu	Ile	Ser
				260				265						270	
Leu	Lys	Asp	Asp	Ala	Asp	Ile	Glu	Gly	Gly	Lys	Leu	Thr	Asp	Thr	Glu
				275				280						285	
Ile	Lys	Ala	Leu	Leu	Leu	Asn	Leu	Phe	Ala	Ala	Gly	Thr	Asp	Thr	Ser
				290				295						300	
Ser	Ser	Thr	Val	Glu	Trp	Ala	Ile	Ala	Glu	Leu	Ile	Arg	His	Pro	Gln
				305				310						320	
Ile	Leu	Lys	Gln	Ala	Arg	Glu	Glu	Ile	Asp	Ala	Val	Val	Gly	Gln	Asp
				325				330						335	
Arg	Leu	Val	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Leu	Thr	Tyr	Leu	Gln	Ala
				340				345						350	
Leu	Val	Lys	Glu	Val	Phe	Arg	Leu	His	Pro	Ser	Thr	Pro	Leu	Ser	Leu
				355				360						365	
Pro	Arg	Ile	Ser	Ser	Glu	Ser	Cys	Glu	Val	Asp	Gly	Tyr	Tyr	Ile	Pro
				370				375						380	
Lys	Gly	Ser	Thr	Leu	Leu	Val	Asn	Val	Trp	Ala	Ile	Ala	Arg	Asp	Pro
				385				390						400	
Lys	Met	Trp	Ala	Asp	Pro	Leu	Glu	Phe	Arg	Pro	Ser	Arg	Phe	Leu	Pro
				405				410						415	
Gly	Gly	Glu	Lys	Pro	Gly	Ala	Asp	Val	Arg	Gly	Asn	Asp	Phe	Glu	Val
				420				425						430	
Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Met	Ser	Leu	Gly
				435				440						445	
Leu	Arg	Met	Val	Gln	Leu	Leu	Ile	Ala	Thr	Leu	Val	Gln	Thr	Phe	Asp
				450				455						460	
Trp	Glu	Leu	Ala	Asn	Gly	Leu	Glu	Pro	Glu	Met	Leu	Asn	Met	Glu	Glu
				465				470						475	
Ala	Tyr	Gly	Leu	Thr	Leu	Gln	Arg	Ala	Ala	Pro	Leu	Met	Val	His	Pro
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Lys	Pro	Arg	Leu	Ala	Pro	His	Val	Tyr	Glu	Ser	Ile				
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					Met	Ser	Pro	
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tta	gcc	ttg	atg	atc	ata	agt	acc	tta	ttt	ctc	cta	tac	cac	163
Leu	Ala	Leu	Met	Ile	Ile	Ser	Thr	Leu	Leu	Gly	Phe	Leu	Tyr	His
								5	10				15	

tct ctt cgc tta cta ctc ttc tcc ggc caa ggt cgc cga cta cta cca 211

Ser	Leu	Arg	Leu	Leu	Leu	Phe	Ser	Gly	Gln	Gly	Arg	Arg	Leu	Leu	Pro	
20					25				30						35	
cca	ggc	cca	cgc	ccg	tgg	ccg	ctg	gtg	gga	aat	ctc	ccg	cac	tta	ggc	259
Pro	Gly	Pro	Arg	Pro	Trp	Pro	Leu	Val	Gly	Asn	Leu	Pro	His	Leu	Gly	
					40				45					50		
ccg	aag	cca	cac	gcc	tcc	atg	gcc	gag	ctc	gct	cga	gcc	tac	gga	ccc	307
Pro	Lys	Pro	His	Ala	Ser	Met	Ala	Glu	Leu	Ala	Arg	Ala	Tyr	Gly	Pro	
					55				60					65		
ctc	atg	cac	cta	aag	atg	ggg	tcc	gtc	cac	gtc	gtg	gtg	gct	tcg	tcg	355
Leu	Met	His	Leu	Lys	Met	Gly	Phe	Val	His	Val	Val	Val	Ala	Ser	Ser	
					70				75					80		
gcg	agc	gcf	gcf	gag	cag	tgc	ctg	agg	gtt	cac	gac	gcf	aat	ttc	ttg	403
Ala	Ser	Ala	Ala	Glu	Gln	Cys	Leu	Arg	Val	His	Asp	Ala	Asn	Phe	Leu	
					85				90					95		
agc	agg	cca	ccc	aac	tcc	ggc	gcc	aag	cac	gtc	gct	tac	aac	tac	gag	451
Ser	Arg	Pro	Pro	Asn	Ser	Gly	Ala	Lys	His	Val	Ala	Tyr	Asn	Tyr	Glu	
					100				105					110		115
gac	ttg	gtt	tcc	aga	ccg	tac	ggf	ccc	aag	tgg	agg	ctg	ttg	agg	aag	499
Asp	Leu	Val	Phe	Arg	Pro	Tyr	Gly	Pro	Lys	Trp	Arg	Leu	Arg	Lys		
					120				125					130		
ata	tgc	gct	cag	cat	att	tcc	tcc	gtc	aag	gct	atg	gat	gac	ttc	agg	547
Ile	Cys	Ala	Gln	His	Ile	Phe	Ser	Val	Lys	Ala	Met	Asp	Asp	Phe	Arg	
					135				140					145		
cgc	gtc	aga	gag	gaa	gag	gtg	gcc	atc	ctg	agt	cgc	gct	cta	gca	ggc	595
Arg	Val	Arg	Glu	Glu	Glu	Val	Ala	Ile	Leu	Ser	Arg	Ala	Leu	Ala	Gly	
					150				155					160		
aaa	agg	gcc	gta	ccc	ata	ggc	caa	atg	ctc	aac	gtg	tgc	gcc	aca	aac	643
Lys	Arg	Ala	Val	Pro	Ile	Gly	Gln	Met	Leu	Asn	Val	Cys	Ala	Thr	Asn	
					165				170					175		
gcc	cta	tct	cgc	gtc	atg	atg	ggg	cgf	cgf	gtg	gtg	ggc	cac	gcf	gat	691
Ala	Leu	Ser	Arg	Val	Met	Met	Gly	Arg	Arg	Val	Val	Gly	His	Ala	Asp	
					180				185					190		195
gga	acc	aac	gac	gcc	aag	gcf	gag	gag	tcc	aaa	gcc	atg	gtc	gtc	gag	739
Gly	Thr	Asn	Asp	Ala	Lys	Ala	Glu	Glu	Phe	Lys	Ala	Met	Val	Val	Glu	
					200				205					210		
ctc	atg	gtc	ctc	tcc	ggc	gtc	tcc	aac	atc	ggf	gat	ttc	atc	ccc	ttc	787
Leu	Met	Val	Leu	Ser	Gly	Val	Phe	Asn	Ile	Gly	Asp	Phe	Ile	Pro	Phe	
					215				220					225		
ctc	gag	cct	ctc	gac	ttg	cag	gga	gtg	gct	tcc	aag	atg	aag	aaa	ctc	835
Leu	Glu	Pro	Leu	Asp	Leu	Gln	Gly	Val	Ala	Ser	Lys	Met	Lys	Lys	Leu	
					230				235					240		
cac	gcf	cgf	ttc	gat	gca	ttc	ttg	acc	gag	att	gta	cga	gag	cgt	tgt	883
His	Ala	Arg	Phe	Asp	Ala	Phe	Leu	Thr	Glu	Ile	Val	Arg	Glu	Arg	Cys	
					245				250					255		
cat	ggg	cag	atc	aac	aac	agt	ggf	gct	cat	cag	gat	gat	ttg	ctt	agc	931
His	Gly	Gln	Ile	Asn	Asn	Ser	Gly	Ala	His	Gln	Asp	Asp	Leu	Leu	Ser	
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acg ttg att tcg ttc aaa ggg ctt gac gat ggc gat ggt tcc agg ctc	979
Thr Leu Ile Ser Phe Lys Gly Leu Asp Asp Gly Asp Gly Ser Arg Leu	
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290	
act gac aca gaa atc aag gcg ctg ctc ttg aac ctt ttg gac acg acg	1027
Thr Asp Thr Glu Ile Lys Ala Leu Leu Asn Leu Leu Asp Thr Thr	
295	300
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tcg agc acg gtg gaa tgg gcc gta gcc gaa ctc cta cgc cac cct aag	1075
Ser Ser Thr Val Glu Trp Ala Val Ala Glu Leu Leu Arg His Pro Lys	
310	315
320	
aca tta gcc caa gtc cgg caa gag ctc gac tcg gtc gtg ggt aag aac	1123
Thr Leu Ala Gln Val Arg Gln Glu Leu Asp Ser Val Val Gly Lys Asn	
325	330
335	
agg ctc gtg tcc gag acc gat ctg aat cag ctg ccc tat cta caa gct	1171
Arg Leu Val Ser Glu Thr Asp Leu Asn Gln Leu Pro Tyr Leu Gln Ala	
340	345
350	355
gtc gtc aaa gaa act ttc cgc ctc cat cct ccg acg ccg ctc tct cta	1219
Val Val Lys Glu Thr Phe Arg Leu His Pro Pro Thr Pro Leu Ser Leu	
360	365
370	
ccg aga ctc gcg gaa gat gat tgc gag atc gac gga tac ctc atc ccc	1267
Pro Arg Leu Ala Glu Asp Asp Cys Glu Ile Asp Gly Tyr Leu Ile Pro	
375	380
385	
aag ggc tcg acc ctt ctg gtg aac gtt tgg gcc ata gcc cgc gat ccc	1315
Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro	
390	395
400	
aag gtt tgg gcc gat ccg ttg gag ttt agg ccc gaa cga ttc ttg acg	1363
Lys Val Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe Leu Thr	
405	410
415	
ggc gga gaa aag gcc gac gtc gat gtc aag ggg aac gat ttc gaa gtg	1411
Gly Gly Glu Lys Ala Asp Val Asp Val Lys Gly Asn Asp Phe Glu Val	
420	425
430	435
ata ccg ttc ggg gcg ggt cgt agg atc tgc gct ggc gtt ggc ttg gga	1459
Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Val Gly Leu Gly	
440	445
450	
ata cgt atg gtc caa ctg ttg acg gcg agt ttg atc cat gca ttc gat	1507
Ile Arg Met Val Gln Leu Leu Thr Ala Ser Leu Ile His Ala Phe Asp	
455	460
465	
ctg gac ctt gct aat ggg ctt ttg gcc caa aat ctg aac atg gaa gaa	1555
Leu Asp Leu Ala Asn Gly Leu Leu Ala Gln Asn Leu Asn Met Glu Glu	
470	475
480	
gca tat ggg ctt acg cta caa cgg gct gag cct ttg ttg gtc cac cct	1603
Ala Tyr Gly Leu Thr Leu Gln Arg Ala Glu Pro Leu Leu Val His Pro	
485	490
495	
agg ccg cgg ttg gcc act cat gtc tat taa ttaaaatttagg cctaaactac	1653
Arg Pro Arg Leu Ala Thr His Val Tyr	
500	505
gatgaatgac ccatttaacg ttaataagag tttcaattt atgtgagttt gcatggatg 1713	
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1815

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<212> PRT
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Leu Leu Pro Pro Gly Pro Arg Pro Trp Pro Leu Val Gly Asn Leu Pro
35 40 45
His Leu Gly Pro Lys Pro His Ala Ser Met Ala Glu Leu Ala Arg Ala
50 55 60
Tyr Gly Pro Leu Met His Leu Lys Met Gly Phe Val His Val Val Val
65 70 75 80
Ala Ser Ser Ala Ser Ala Ala Glu Gln Cys Leu Arg Val His Asp Ala
85 90 95
Asn Phe Leu Ser Arg Pro Pro Asn Ser Gly Ala Lys His Val Ala Tyr
100 105 110
Asn Tyr Glu Asp Leu Val Phe Arg Pro Tyr Gly Pro Lys Trp Arg Leu
115 120 125
Leu Arg Lys Ile Cys Ala Gln His Ile Phe Ser Val Lys Ala Met Asp
130 135 140
Asp Phe Arg Arg Val Arg Glu Glu Glu Val Ala Ile Leu Ser Arg Ala
145 150 155 160
Leu Ala Gly Lys Arg Ala Val Pro Ile Gly Gln Met Leu Asn Val Cys
165 170 175
Ala Thr Asn Ala Leu Ser Arg Val Met Met Gly Arg Arg Val Val Gly
180 185 190

His Ala Asp Gly Thr Asn Asp Ala Lys Ala Glu Glu Phe Lys Ala Met
195 200 205
Val Val Glu Leu Met Val Leu Ser Gly Val Phe Asn Ile Gly Asp Phe
210 215 220
Ile Pro Phe Leu Glu Pro Leu Asp Leu Gln Gly Val Ala Ser Lys Met
225 230 235 240
Lys Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Glu Ile Val Arg
245 250 255
Glu Arg Cys His Gly Gln Ile Asn Asn Ser Gly Ala His Gln Asp Asp
260 265 270
Leu Leu Ser Thr Leu Ile Ser Phe Lys Gly Leu Asp Asp Gly Asp Gly
275 280 285
Ser Arg Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Asn Leu Leu
290 295 300
Asp Thr Thr Ser Ser Thr Val Glu Trp Ala Val Ala Glu Leu Leu Arg
305 310 315 320
His Pro Lys Thr Leu Ala Gln Val Arg Gln Glu Leu Asp Ser Val Val
325 330 335
Gly Lys Asn Arg Leu Val Ser Glu Thr Asp Leu Asn Gln Leu Pro Tyr
340 345 350
Leu Gln Ala Val Val Lys Glu Thr Phe Arg Leu His Pro Pro Thr Pro
355 360 365
Leu Ser Leu Pro Arg Leu Ala Glu Asp Asp Cys Glu Ile Asp Gly Tyr
370 375 380
Leu Ile Pro Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala
385 390 395 400
Arg Asp Pro Lys Val Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg
405 410 415
Phe Leu Thr Gly Gly Glu Lys Ala Asp Val Asp Val Lys Gly Asn Asp
420 425 430

Phe	Glu	Val	Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Val
			435				440					445			
Gly	Leu	Gly	Ile	Arg	Met	Val	Gln	Leu	Leu	Thr	Ala	Ser	Leu	Ile	His
	450				455			455			460				
Ala	Phe	Asp	Leu	Asp	Leu	Ala	Asn	Gly	Leu	Leu	Ala	Gln	Asn	Leu	Asn
	465				470				475			475			480
Met	Glu	Glu	Ala	Tyr	Gly	Leu	Thr	Leu	Gln	Arg	Ala	Glu	Pro	Leu	Leu
					485			490			495				
Val	His	Pro	Arg	Pro	Arg	Leu	Ala	Thr	His	Val	Tyr				
					500			505							

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<211> 1824

<212> DNA

<213> Jap. Morning Glory

<220>

<221> CDS

<222> (2)..(1555)

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Ser	Leu	Thr	Leu	Ile	Phe	Cys	Thr	Leu	Val	Phe	Ala	Ile	Phe	Leu	Tyr	
1				5					10						15	

ttt	ctt	att	ctc	agg	gtg	aaa	cag	cgt	tac	cct	cct	ctc	cca	ccc		97
Phe	Leu	Ile	Leu	Arg	Val	Lys	Gln	Arg	Tyr	Pro	Leu	Pro	Leu	Pro		
						20				25			30			

gga	cca	aaa	cca	tgg	ccg	gtg	tta	gga	aac	ctt	ccc	cac	ctg	ggc	aag	145
Gly	Pro	Lys	Pro	Trp	Pro	Val	Leu	Gly	Asn	Leu	Pro	His	Leu	Gly	Lys	
							35		40			45				

aag	cct	cac	cag	tcg	att	gcg	gcc	atg	gct	gag	agg	tac	ggc	ccc	ctc	193
Lys	Pro	His	Gln	Ser	Ile	Ala	Ala	Met	Ala	Glu	Arg	Tyr	Gly	Pro	Leu	
						50		55		60						

atg	cac	ctc	cgc	cta	gga	ttc	gtg	gac	gtg	gtt	gtg	gcc	gcc	tcc	gcc	241
Met	His	Leu	Arg	Leu	Gly	Phe	Val	Asp	Val	Val	Val	Ala	Ala	Ser	Ala	
						65		70		75		80				

gcc	gtg	gcc	gct	cag	ttc	ttg	aaa	gtt	cac	gac	tcg	aac	ttc	tcc	aac	289
Ala	Val	Ala	Ala	Gln	Phe	Leu	Lys	Val	His	Asp	Ser	Asn	Phe	Ser	Asn	
						85		90		95						

cgg	ccg	ccg	aac	tcc	ggc	gcg	gaa	cac	att	gct	tat	aac	tat	caa	gac	337
Arg	Pro	Pro	Asn	Ser	Gly	Ala	Glu	His	Ile	Ala	Tyr	Asn	Tyr	Gln	Asp	
						100		105		110						

ctc	gtc	ttc	qcg	ccc	tac	ggc	ccg	cg	tgg	cg	atg	ctt	agg	aag	atc	385
Leu	Val	Phe	Ala	Pro	Tyr	Gly	Pro	Arg	Trp	Arg	Met	Leu	Arg	Lys	Ile	
						115		120		125						

acc	tcc	gtg	cat	ctc	ttc	tcg	gcc	aag	gct	ttg	gat	gac	ttc	tgc	cat	433
Thr	Ser	Val	His	Leu	Phe	Ser	Ala	Lys	Ala	Leu	Asp	Asp	Phe	Cys	His	
						130		135		140						

gtt	cg	c	c	c	g	a	g	g	g	act	ctg	aca	cg	agt	ct	481
Val	Arg	Gln	Glu	Glu	Val	Ala	Thr	Leu	Thr	Arg	Ser	Leu	Ala	Ser	Ala	
						145		150		155		160				

ggc	aaa	act	cca	gta	aaa	cta	ggg	cag	tta	cta	aac	gtg	tgc	acc	acg	529
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Glu	Phe	Asn	Pro	His	Arg	Phe	Leu	Pro	Gly	Gly	Glu	Lys	Pro	Asn	Val	
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gat att aaa ggg aat gac ttt gaa gtg att cct ttt gga gcc ggg cgt															1345	
Asp	Ile	Lys	Gly	Asn	Asp	Phe	Glu	Val	Ile	Pro	Phe	Gly	Ala	Gly	Arg	
435								440					445			
aga	ata	tgc	tct	ggg	atg	agt	ttg	ggg	ata	agg	atg	gtt	cac	ctg	ttg	1393
Arg	Ile	Cys	Ser	Gly	Met	Ser	Leu	Gly	Ile	Arg	Met	Val	His	Leu	Leu	
450								455					460			
gtt	gca	act	ttg	gtg	cat	gct	ttt	gat	ttg	gtg	aat	gga	caa		1441	
Val	Ala	Thr	Leu	Val	His	Ala	Phe	Asp	Trp	Asp	Leu	Val	Asn	Gly	Gln	
465							470					475			480	
tct	gta	gag	acg	ctc	aat	atg	gag	gaa	gct	tat	ggt	ctc	acc	ctt	caa	1489
Ser	Val	Glu	Thr	Leu	Asn	Met	Glu	Glu	Ala	Tyr	Gly	Leu	Thr	Leu	Gln	
485								490						495		
cga	gct	gtt	cct	ttg	atg	ttg	cat	cca	aag	ccc	aga	tta	caa	cca	cat	1537
Arg	Ala	Val	Pro	Leu	Met	Leu	His	Pro	Lys	Pro	Arg	Leu	Gln	Pro	His	
500								505						510		
ctc	tat	act	ctc	aat	taa	attgcaattt	gattttggtg	attatacaat								1585
Leu	Tyr	Thr	Leu	Asn												
515																
tataatcgag	ggacatagga	tccccattta	tttatattca	gttataagag	acttccaaca											1645
aaggcttagc	tttcgacctt	aaaagttgta	aaagagggcc	tacatatgt	aaagccgc											1705
aaaggaaaaac	tggttgtatt	caattccgct	aggccttgc	cgaaagacct	catgaagact											1765
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1					5				10				15			
Phe	Leu	Ile	Leu	Arg	Val	Lys	Gln	Arg	Tyr	Pro	Leu	Pro	Leu	Pro	Pro	
				20				25				30				
Gly	Pro	Lys	Pro	Trp	Pro	Val	Leu	Gly	Asn	Leu	Pro	His	Leu	Gly	Lys	
				35				40				45				
Lys	Pro	His	Gln	Ser	Ile	Ala	Ala	Met	Ala	Glu	Arg	Tyr	Gly	Pro	Leu	
				50				55				60				
Met	His	Leu	Arg	Leu	Gly	Phe	Val	Asp	Val	Val	Val	Ala	Ala	Ser	Ala	
				65				70				75			80	
Ala	Val	Ala	Ala	Gln	Phe	Leu	Lys	Val	His	Asp	Ser	Asn	Phe	Ser	Asn	
				85				90				95				
Arg	Pro	Pro	Asn	Ser	Gly	Ala	Glu	His	Ile	Ala	Tyr	Asn	Tyr	Gln	Asp	
				100				105				110				
<u>Leu</u>	<u>Val</u>	<u>Phe</u>	<u>Ala</u>	<u>Pro</u>	<u>Tyr</u>	<u>Gly</u>	<u>Pro</u>	<u>Arg</u>	<u>Trp</u>	<u>Arg</u>	<u>Met</u>	<u>Leu</u>	<u>Arg</u>	<u>Lys</u>	<u>Ile</u>	
				115				120				125				
Thr	Ser	Val	His	Leu	Phe	Ser	Ala	Lys	Ala	Leu	Asp	Asp	Phe	Cys	His	
				130				135				140				
Val	Arg	Gln	Glu	Glu	Val	Ala	Thr	Leu	Thr	Arg	Ser	Leu	Ala	Ser	Ala	
				145				150				155			160	

Gly Lys Thr Pro Val Lys Leu Gly Gln Leu Leu Asn Val Cys Thr Thr
 165 170 175
 Asn Ala Leu Ala Arg Val Met Leu Gly Arg Lys Val Phe Asn Asp Gly
 180 185 190
 Gly Ser Lys Ser Asp Pro Lys Ala Glu Glu Phe Lys Ser Met Val Glu
 195 200 205
 Glu Met Met Val Leu Ala Gly Ser Phe Asn Ile Gly Asp Phe Ile Pro
 210 215 220
 Val Leu Gly Trp Phe Asp Val Gln Gly Ile Val Gly Lys Met Lys Lys
 225 230 235 240
 Leu His Ala Arg Phe Asp Ala Phe Leu Asn Thr Ile Leu Glu Glu His
 245 250 255
 Lys Cys Val Asn Asn Gln His Thr Thr Leu Ser Lys Asp Val Asp Phe
 260 265 270
 Leu Ser Thr Leu Ile Arg Leu Lys Asp Asn Gly Ala Asp Met Asp Cys
 275 280 285
 Glu Glu Gly Lys Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn
 290 295 300
 Leu Phe Thr Ala Gly Thr Asp Thr Ser Ser Thr Val Glu Trp Ala
 305 310 315 320
 Ile Ala Glu Leu Leu Arg Asn Pro Lys Ile Leu Asn Gln Ala Gln Gln
 325 330 335
 Glu Leu Asp Leu Val Val Gly Gln Asn Gln Leu Val Thr Glu Ser Asp
 340 345 350
 Leu Thr Asp Leu Pro Phe Leu Gln Ala Ile Val Lys Glu Thr Phe Arg
 355 360 365
 Leu His Pro Ser Thr Pro Leu Ser Leu Pro Arg Met Gly Ala Gln Gly
 370 375 380
 Cys Glu Ile Asn Gly Tyr Ile Pro Lys Gly Ala Thr Leu Leu Val
 385 390 395 400
 Asn Val Trp Ala Ile Ala Arg Asp Pro Asn Val Trp Thr Asn Pro Leu
 405 410 415
 Glu Phe Asn Pro His Arg Phe Leu Pro Gly Gly Glu Lys Pro Asn Val
 420 425 430
 Asp Ile Lys Gly Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg
 435 440 445
 Arg Ile Cys Ser Gly Met Ser Leu Gly Ile Arg Met Val His Leu Leu
 450 455 460
 Val Ala Thr Leu Val His Ala Phe Asp Trp Asp Leu Val Asn Gly Gln
 465 470 475 480
 Ser Val Glu Thr Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln
 485 490 495
 Arg Ala Val Pro Leu Met Leu His Pro Lys Pro Arg Leu Gln Pro His
 500 505 510
 Leu Tyr Thr Leu Asn
 515

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 <211> 1667
 <212> DNA
 <213> Gentian

<220>
 <221> CDS
 <222> (1)..(1431)

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 1 5 10 15

 ctc gcg gaa atg gcg aaa acc tac ggt ccg ctc atg cac ttg aag ttc 96

Ser	Ser	Ser	Thr	Val	Glu	Trp	Ala	Met	Ala	Glu	Leu	Ile	Arg	Asn	Pro			
275				280								285						
aag	tta	cta	gtc	caa	gcc	caa	gaa	gag	cta	gac	aga	gtt	gtc	ggg	ccg		912	
Lys	Leu	Leu	Val	Gln	Ala	Gln	Glu	Glu	Leu	Asp	Arg	Val	Val	Gly	Pro			
290				295								300						
aac	cga	ttc	gtt	acc	gaa	tct	gat	ctt	cct	caa	ctg	aca	ttc	ctt	caa		960	
Asn	Arg	Phe	Val	Thr	Glu	Ser	Asp	Leu	Pro	Gln	Leu	Thr	Phe	Leu	Gln			
305				310							315				320			
gcc	gtc	atc	aaa	gag	act	ttc	agg	ctt	cat	cca	tcc	acc	cca	ctc	tct		1008	
Ala	Val	Ile	Lys	Glu	Thr	Phe	Arg	Leu	His	Pro	Ser	Thr	Pro	Leu	Ser			
325				330											335			
ctt	cca	cga	atg	gcg	gcg	gag	gac	tgt	gag	atc	aat	ggg	tat	tat	gtc		1056	
Leu	Pro	Arg	Met	Ala	Ala	Glu	Asp	Cys	Glu	Ile	Asn	Gly	Tyr	Tyr	Val			
340				345								350						
tca	gaa	ggt	tcg	aca	ttg	ctc	gtc	aat	gtg	tgg	gcc	ata	gct	cgt	gat		1104	
Ser	Glu	Gly	Ser	Thr	Leu	Leu	Val	Asn	Val	Trp	Ala	Ile	Ala	Arg	Asp			
355				360								365						
cca	aat	gct	tgg	gcc	aat	cca	cta	gat	ttc	aac	ccg	act	cgt	ttc	ttg		1152	
Pro	Asn	Ala	Trp	Ala	Asn	Pro	Leu	Asp	Phe	Asn	Pro	Thr	Arg	Phe	Leu			
370				375							380							
gcc	ggt	gga	gag	aag	cct	aat	gtt	gat	gtt	aaa	ggg	aat	gat	ttt	gaa		1200	
Ala	Gly	Gly	Glu	Lys	Pro	Asn	Val	Asp	Val	Lys	Gly	Asn	Asp	Phe	Glu			
385				390						395					400			
gtg	ata	cct	ttc	ggt	gct	ggg	cgc	agg	ata	tgt	gcc	gga	atg	agc	tta		1248	
Val	Ile	Pro	Phe	Gly	Ala	Gly	Arg	Arg	Ile	Cys	Ala	Gly	Met	Ser	Leu			
405				410											415			
ggt	ata	ccg	atg	gtt	caa	cta	gta	acg	gct	tcg	tta	gtt	cat	tcg	ttt		1296	
Gly	Ile	Arg	Met	Val	Gln	Leu	Val	Thr	Ala	Ser	Leu	Val	His	Ser	Phe			
420				425								430						
gat	tgg	gct	ttg	ttg	gat	gga	ctt	aaa	ccc	gag	aag	ctt	gac	atg	gag		1344	
Asp	Trp	Ala	Leu	Leu	Asp	Gly	Leu	Lys	Pro	Glu	Lys	Leu	Asp	Met	Glu			
435				440								445						
gaa	ggt	tat	gga	cta	acg	ctt	caa	cga	gct	tca	cct	tta	atc	gtc	cat		1392	
Glu	Gly	Tyr	Gly	Leu	Thr	Leu	Gln	Arg	Ala	Ser	Pro	Leu	Ile	Val	His			
450				455								460						
cca	aag	ccg	agg	ctc	tcg	gct	caa	gtt	tat	tgt	atg	taa	caagtttg			1441		
Pro	Lys	Pro	Arg	Leu	Ser	Ala	Gln	Val	Tyr	Cys	Met							
465				470							475							
aagccagtct	gatttcagtt	ggatttttag	ttat	ttat	ttat	ttat	ttat	ttat	ttat	ttat	ttat	ttat	ttat	ttat	ttat		1501	
gtat	ttttcggt	tgaata	caat	aaaggaa	agg	tggat	cgct	gtct	gtct	gtct	gtct	gtct	gtct	gtct	gtct		1561	
taacgtgtt	tgat	agt	tacc	gtgt	tttact	aaa	acg	atgt	cg	tttg	attt	tttat	atgt	atgt	atgt		1621	
taaaaaaaaata	aac	ag	ctg	gga	ttt	ga	acca	aaaa	aaaa	aaaa	aaaa	aaaa	aaaa	aaaa	aaaa		1667	

<210> 23
<211> 476
<212> PRT
<213> Gentian

<400> 23

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Leu Ala Glu Met Ala Lys Thr Tyr Gly Pro Leu Met His Leu Lys Phe
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Gly Leu Lys Asp Ala Val Val Ala Ser Ser Ala Ser Val Ala Glu Gln
35 40 45
Phe Leu Lys His Asp Val Asn Phe Ser Asn Arg Pro Pro Asn Ser
50 55 60
Gly Ala Lys His Ile Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro
65 70 75 80
Tyr Gly Pro Arg Trp Arg Leu Leu Arg Lys Ile Cys Ser Val His Leu
85 90 95
Phe Ser Ser Lys Ala Leu Asp Asp Phe Gln His Val Arg His Glu Glu
100 105 110
Ile Cys Ile Leu Ile Arg Ala Ile Ala Ser Gly Gly His Ala Pro Val
115 120 125
Asn Leu Gly Lys Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg
130 135 140

Val Met Leu Gly Arg Arg Val Phe Glu Gly Asp Gly Gly Glu Asn Pro
145 150 155 160
His Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala
165 170 175
Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Val Leu Asp Trp Phe Asp
180 185 190
Leu Gln Gly Ile Ala Gly Lys Met Lys Lys Leu His Ala Arg Phe Asp
195 200 205
Lys Phe Leu Asn Gly Ile Leu Glu Asp Arg Lys Ser Asn Gly Ser Asn
210 215 220
Gly Ala Glu Gln Tyr Val Asp Leu Leu Ser Val Leu Ile Ser Leu Gln
225 230 235 240
Asp Ser Asn Ile Asp Gly Gly Asp Glu Gly Thr Lys Leu Thr Asp Thr
245 250 255
Glu Ile Lys Ala Leu Leu Asn Leu Phe Ile Ala Gly Thr Asp Thr
260 265 270
Ser Ser Ser Thr Val Glu Trp Ala Met Ala Glu Leu Ile Arg Asn Pro
275 280 285
Lys Leu Leu Val Gln Ala Gln Glu Glu Leu Asp Arg Val Val Gly Pro
290 295 300
Asn Arg Phe Val Thr Glu Ser Asp Leu Pro Gln Leu Thr Phe Leu Gln
305 310 315 320
Ala Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser
325 330 335
Leu Pro Arg Met Ala Ala Glu Asp Cys Glu Ile Asn Gly Tyr Tyr Val
340 345 350
Ser Glu Gly Ser Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp
355 360 365
Pro Asn Ala Trp Ala Asn Pro Leu Asp Phe Asn Pro Thr Arg Phe Leu
370 375 380
Ala Gly Gly Glu Lys Pro Asn Val Asp Val Lys Gly Asn Asp Phe Glu
385 390 395 400
Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu
405 410 415
Gly Ile Arg Met Val Gln Leu Val Thr Ala Ser Leu Val His Ser Phe
420 425 430
Asp Trp Ala Leu Leu Asp Gly Leu Lys Pro Glu Lys Leu Asp Met Glu
435 440 445
Glu Gly Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His
450 455 460
Pro Lys Pro Arg Leu Ser Ala Gln Val Tyr Cys Met
465 470 475

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<211> 1214
<212> DNA
<213> Lisianthus

<220>
<221> CDS
<222> (2)..(1093)

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1 5 10 15

tta ggt caa tta ctc ggg gtg tgt acc aca aat gct ctg gcg aga gtg 97
Leu Gly Gln Leu Leu Gly Val Cys Thr Thr Asn Ala Leu Ala Arg Val
20 25 30

atg ctt gga agg agg gta ttc ggc gat ggg agc ggc gta gat cct 145
Met Leu Gly Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Val Asp Pro
35 40 45

cag gcg gac gag ttc aaa tcc atg gtg gtg gaa atc atg gtg ttg gcc 193
Gln Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala
50 55 60

ggc gcg ttt aat cta ggt gat ttt att ccc gct ctt gat tgg ttc gat 241
Gly Ala Phe Asn Leu Gly Asp Phe Ile Pro Ala Leu Asp Trp Phe Asp
65 70 75 80

ctg cag gga att acg gca aaa atg aag aaa gtt cac gct cgt ttc gat 289
Leu Gln Gly Ile Thr Ala Lys Met Lys Lys Val His Ala Arg Phe Asp
85 90 95

gcg ttc tta gac gcg atc ctt gag gag cac aaa tcc aac ggc tct cgc 337
Ala Phe Leu Asp Ala Ile Leu Glu Glu His Lys Ser Asn Gly Ser Arg
100 105 110

gga gct aag caa cac gtt gac ttg ctg agt atg ttg atc tcc ctt caa 385
Gly Ala Lys Gln His Val Asp Leu Leu Ser Met Leu Ile Ser Leu Gln
115 120 125

gat aat aac att gat ggt gaa agt ggc gcc aaa ctc act gat aca gaa 433
Asp Asn Asn Ile Asp Gly Glu Ser Gly Ala Lys Leu Thr Asp Thr Glu
130 135 140

atc aaa gct ttg ctt ctg aac ttg ttc acg gct gga aca gac acg tca 481
Ile Lys Ala Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Ser
145 150 155 160

tca agt act gtg gag tgg gca atc gca gag cta atc cga aac cca gaa 529
Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn Pro Glu
165 170 175

gta ttg gtt caa gcc caa caa gag ctc gat aga gta gtt ggg cca agt 577
Val Leu Val Gln Ala Gln Gln Glu Leu Asp Arg Val Val Gly Pro Ser
180 185 190

cgt ctt gtg acc gaa tct gat ctg cct caa ttg gca ttc ctt caa gct 625
Arg Leu Val Thr Glu Ser Asp Leu Pro Gln Leu Ala Phe Leu Gln Ala
195 200 205

gtc atc aaa gag act ttc aga ctt cat cca tcc act cca ctc tct ctt 673

Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu
 210 215 220
 cca cga atg gct tca gag ggt tgt gaa atc aat gga tac tcc atc cca 721
 Pro Arg Met Ala Ser Glu Gly Cys Glu Ile Asn Gly Tyr Ser Ile Pro
 225 230 235 240
 aag ggt tcg aca ttg ctc gtt aac gta tgg tcc ata gcc cgt gat cct 769
 Lys Gly Ser Thr Leu Leu Val Asn Val Trp Ser Ile Ala Arg Asp Pro
 245 250 255
 agt ata tgg gcc gac cca tta gaa ttt agg ccg gca cgt ttc ttg ccc 817
 Ser Ile Trp Ala Asp Pro Leu Glu Phe Arg Pro Ala Arg Phe Leu Pro
 260 265 270
 ggc gga gaa aag ccc aat gtt gat gtg aga ggc aat gat ttt gag gtc 865
 Gly Gly Glu Lys Pro Asn Val Asp Val Arg Gly Asn Asp Phe Glu Val
 275 280 285
 ata cca ttt ggt gct gga cgt agg ata tgg gct gga atg agc ttg ggt 913
 Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Ser Leu Gly
 290 295 300
 tta aga atg gtt caa ctt tcg aca gct act ttg gtt cat tcg ttt aat 961
 Leu Arg Met Val Gln Leu Ser Thr Ala Thr Leu Val His Ser Phe Asn
 305 310 315 320
 tgg gat ttg ctg aat ggg atg agc cca gat aaa ctt gac atg gaa gaa 1009
 Trp Asp Leu Leu Asn Gly Met Ser Pro Asp Lys Leu Asp Met Glu Glu
 325 330 335
 gct tat ggg ctt aca ttg caa cgg gct tca cct ttg att gtc cac cca 1057
 Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ser Pro Leu Ile Val His Pro
 340 345 350
 aag ccc agg ctt gct agc tct atg tat gtt aaa tga aattatgctg 1103
 Lys Pro Arg Leu Ala Ser Ser Met Tyr Val Lys
 355 360
 tgcgaataat tccttattta tagcaggaaa tgtcatcttg aattatgtgt aatgttcttc 1163
 taacttcga tggaaagtgc aaaaaaaaaaaaaaaa a 1214

 <210> 25
 <211> 363
 <212> PRT
 <213> Lisianthus

 <400> 25
 Arg Ile Leu Thr Arg Ser Ile Ala Ser Ala Gly Glu Asn Pro Ile Asn
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 20 25 30
 Met Leu Gly Arg Arg Val Phe Gly Asp Gly Ser Gly Gly Val Asp Pro
 35 40 45
 Gln Ala Asp Glu Phe Lys Ser Met Val Val Glu Ile Met Val Leu Ala
 50 55 60
 -Gly-Ala-Phe-Asn-Leu-Gly-Asp-Phe-Ile-Pro-Ala-Leu-Asp-Trp-Phe-Asp-
 65 70 75 80
 Leu Gln Gly Ile Thr Ala Lys Met Lys Lys Val His Ala Arg Phe Asp
 85 90 95
 Ala Phe Leu Asp Ala Ile Leu Glu Glu His Lys Ser Asn Gly Ser Arg
 100 105 110

<210> 26
<211> 1757
<212> DNA
<213> Petunia sp.

<220>
<221> CDS
<222> (35) .. (1525)

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Met Asp Tyr Val Asn Ile Leu
1 5

ctg gga ctg ttt ttc act tgg ttc ttg gtg aat gga ctc atg tca ctt 103
 Leu Gly Leu Phe Phe Thr Trp Phe Leu Val Asn Gly Leu Met Ser Leu
 10 15 20

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cga aga aga aaa atc tct aag aaa ctt cca cca ggt cca ttt cct ttg 151
Arg Arg Arg Lys Ile Ser Lys Lys Leu Pro Pro Gly Pro Phe Pro Leu
      25          30          35

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cct atc atc gga aat ctt cac tta ctt ggt aat cat cct cac aaa tca 199
Pro Ile Ile Gly Asn Leu His Leu Leu Gly Asn His Pro His Lys Ser
 40 45 50 55

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ctt gct caa ctt gca aaa att cat ggt cct att atg aat ctc aaa tta 247
Leu Ala Gln Leu Ala Lys Ile His Gly Pro Ile Met Asn Leu Lys Leu
          60           65           70

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ggc caa cta aac aca gtc att tca tca tca gtc gtg gca aga gaa	295
Gly Gln Leu Asn Thr Val Val Ile Ser Ser Ser Val Val Ala Arg Glu	
75	80
	85
gtc ttg caa aaa caa gac tta aca ttt tcc aat agg ttt gtc ccg gac	343
Val Leu Gln Lys Gln Asp Leu Thr Phe Ser Asn Arg Phe Val Pro Asp	
90	95
	100
gta gtc cat gtc cga aat cac tcc gat ttt tct gtt gtt tgg tta cca	391
Val Val His Val Arg Asn His Ser Asp Phe Ser Val Val Trp Leu Pro	
105	110
	115
gtc aat tct cga tgg aaa acg ctt cgc aaa atc atg aac tct agc atc	439
Val Asn Ser Arg Trp Lys Thr Leu Arg Lys Ile Met Asn Ser Ser Ile	
120	125
	130
	135
ttt tct ggt aac aag ctt gat ggt aat caa cat ctg agg tct aaa aag	487
Phe Ser Gly Asn Lys Leu Asp Gly Asn Gln His Leu Arg Ser Lys Lys	
140	145
	150
gtc caa gag tta att gat tat tgt caa aag tgt gcc aag aat ggc gaa	535
Val Gln Glu Leu Ile Asp Tyr Cys Gln Lys Cys Ala Lys Asn Gly Glu	
155	160
	165
gca gtg gat ata gga aga gca act ttt gga act act ttg aat ttg cta	583
Ala Val Asp Ile Gly Arg Ala Thr Phe Gly Thr Thr Leu Asn Leu Leu	
170	175
	180
tcc aac acc att ttc tct aaa gat ttg act aat ccg ttt tct gat tct	631
Ser Asn Thr Ile Phe Ser Lys Asp Leu Thr Asn Pro Phe Ser Asp Ser	
185	190
	195
gct aaa gag ttt aag gaa ttg gtt tgg aac att atg gtt gag gct gga	679
Ala Lys Glu Phe Lys Glu Leu Val Trp Asn Ile Met Val Glu Ala Gly	
200	205
	210
	215
aaa ccc aat ttg gtg gac tac ttt cct ttc ctt gag aaa att gat ccg	727
Lys Pro Asn Leu Val Asp Tyr Phe Pro Phe Leu Glu Lys Ile Asp Pro	
220	225
	230
caa ggt ata aag cga cgc atg act aat aat ttt act aag ttt ctt ggc	775
Gln Gly Ile Lys Arg Arg Met Thr Asn Asn Phe Thr Lys Phe Leu Gly	
235	240
	245
ctt atc agc ggt ttg att gat gac cgg tta aag gaa agg aat cta agg	823
Leu Ile Ser Gly Leu Ile Asp Asp Arg Leu Lys Glu Arg Asn Leu Arg	
250	255
	260
gac aat gca aat att gat gtt tta gac gcc ctt ctc aac att agc caa	871
Asp Asn Ala Asn Ile Asp Val Leu Asp Ala Leu Leu Asn Ile Ser Gln	
265	270
	275
gag aac cca gaa gag att gac agg aat caa atc gag cag ttg tgt ctg	919
Glu Asn Pro Glu Glu Ile Asp Arg Asn Gln Ile Glu Gln Leu Cys Leu	
280	285
	290
	295
gac ttg ttt gca gca ggg act gat act aca tcg aat acc ttg gag tgg	967
Asp Leu Phe Ala Ala Gly Thr Asp Thr Thr Ser Asn Thr Leu Glu Trp	
300	305
	310
gca atg gca gaa cta ctt cag aat cca cac aca ttg cag aaa gca caa	1015
Ala Met Ala Glu Leu Leu Gln Asn Pro His Thr Leu Gln Lys Ala Gln	
315	320
	325

gaa gaa ctt gca caa gtc att ggt aaa ggc aaa caa gta gaa gaa gca Glu Glu Leu Ala Gln Val Ile Gly Lys Gly Lys Gln Val Glu Glu Ala 330 335 340	1063
gat gtt gga cga cta cct tac ttg cga tgc ata gtg aaa gaa acc tta Asp Val Gly Arg Leu Pro Tyr Leu Arg Cys Ile Val Lys Glu Thr Leu 345 350 355	1111
cga ata cac cca gcg gct cct ctc tta att cca cgt aaa gtg gag gaa Arg Ile His Pro Ala Ala Pro Leu Leu Ile Pro Arg Lys Val Glu Glu 360 365 370 375	1159
gac gtt gag ttg tct acc tat att att cca aag gat tca caa gtt cta Asp Val Glu Leu Ser Thr Tyr Ile Ile Pro Lys Asp Ser Gln Val Leu 380 385 390	1207
gtg aac gta tgg gca att gga cgc aac tct gat cta tgg gaa aat cct Val Asn Val Trp Ala Ile Gly Arg Asn Ser Asp Leu Trp Glu Asn Pro 395 400 405	1255
ttg gtc ttt aag cca gaa agg ttt tgg gag tca gaa ata gat atc cga Leu Val Phe Lys Pro Glu Arg Phe Trp Glu Ser Glu Ile Asp Ile Arg 410 415 420	1303
ggt cga gat ttt gaa ctc att cca ttt ggt gct ggt cga aga att tgc Gly Arg Asp Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys 425 430 435	1351
cct gga ttg cct ttg gct atg agg atg att cca gta gca cta ggt tca Pro Gly Leu Pro Leu Ala Met Arg Met Ile Pro Val Ala Leu Gly Ser 440 445 450 455	1399
ttg cta aac tca ttt aat tgg aaa cta tat ggt gga att gca cct aaa Leu Leu Asn Ser Phe Asn Trp Lys Leu Tyr Gly Gly Ile Ala Pro Lys 460 465 470	1447
gat ttg gac atg cag gaa aag ttt ggc att acc ttg gcg aaa gcc caa Asp Leu Asp Met Gln Glu Lys Phe Gly Ile Thr Leu Ala Lys Ala Gln 475 480 485	1495
cct ctg cta gct atc cca act ccc ctg tag ctataggat aaattaagtt Pro Leu Leu Ala Ile Pro Thr Pro Leu 490 495	1545
gaggtttaa gttacttagta gattctattg cagctatagg atttcttca ccatcacgta tgctttaccc ttggatgatg gaaagaaaata tctatagctt tggtttgtt tagttgcac ataaaaattg aatgaatgga ataccatgga gttataagaa ataataagac tatgattctt accctacttg aacaatgaca tggctatttc ac	1605 1665 1725 1757

<210> 27

<211> 18

<212> DNA

<213> Artificial Sequence -----

<220>

<223> Description of Artificial Sequence:oligonucleotide

<400> 27

ttttttttt tttttta

18

<210> 28
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 28

ttttttttt ttttttc

18

<210> 29
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 29

ttttttttt ttttttg

18

<210> 30
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide representing a conserved region in plant cytochrome p450 sequences.

<400> 30

Trp Ala Ile Gly Arg Asp Pro
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<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

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<222> (6)
<223> n is inosine

<220>
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<223> n is inosine

<220>
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<222> (12)
<223> n is inosine

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<220>
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<223> n is inosine

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tgggcnatng gnmngngaycc                                20

<210> 32
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide representing a
conserved region in plant cytochrome p450 sequences.

<400> 32
Phe Arg Pro Glu Arg Phe
    1           5

<210> 33
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<220>
<221> Modified base
<222> (11)
<223> n is inosine

<220>
<221> Modified base
<222> (14)
<223> n is inosine

<220>
<221> Modified base
<222> (20)
<223> n is inosine

<400> 33
agaattymg ncngarmgn tt                                22

<210> 34
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

<220>-----.
<221> Modified base
<222> (3)
<223> n is inosine

<220>

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<221> Modified base
<222> (9)
<223) n is inosine

<220>
<221> Modified base
<222> (12)
<223) n is inosine

<220>
<221> Modified base
<222> (15)
<223) n is inosine

<220>
<221> Modified base
<222> (18)
<223) n is inosine

<220>
<221> Modified base
<222> (21)
<223) n is inosine

<220>
<221> Modified base
<222> (24)
<223) n is inosine

<220>
<221> Modified base
<222> (30)
<223) n is inosine

<400> 34
ccnttyggng cnggnmgnmg natntgkscn gg 32
<210> 35
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide representing a
conserved region in plant cytochrome p450 sequences.

<220>
<221> UNSURE
<222> (3)
<223> Xaa can be any amino acid.

<400> 35
Glu Phe Xaa Pro Glu Arg Phe
 1           5

<210> 36
<211> 20
<212>-DNA-----
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligonucleotide

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<220>
<221> Modified base
<222> (3)
<223> n is inosine

<220>
<221> Modified base
<222> (7)
<223> n is inosine

<220>
<221> Modified base
<222> (8)
<223> n is inosine

<220>
<221> Modified base
<222> (9)
<223> n is inosine

<220>
<221> Modified base
<222> (12)
<223> n is inosine

<220>
<221> Modified base
<222> (15)
<223> n is inosine

<220>
<221> Modified base
<222> (18)
<223> n is inosine

<400> 36
ganttnnncc cnganmgntt

<210> 37
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 37
ccacacgagt agtttgcca tttgaccc

<210> 38
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 38
gtcttggaca tcacacttca atctg

<210> 39
<211> 17
<212> DNA
<213> Artificial Sequence

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20

28

25

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 39
ccgaattccc ccccccc

17

<210> 40
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<220>
<221> Modified base
<222> (3)
<223> n is inosine

<220>
<221> Modified base
<222> (9)
<223> n is inosine

<220>
<221> Modified base
<222> (12)
<223> n is inosine

<220>
<221> Modified base
<222> (18)
<223> n is inosine

<220>
<221> Modified base
<222> (21)
<223> n is inosine

<220>
<221> Modified base
<222> (24)
<223> n is inosine

<220>
<221> Modified base
<222> (30)
<223> n is inosine

<400> 40
ccnggrcana tnckyytncc ngcncraan gg

32

<210> 41
<211> 496
<212> PRT
<213> Petunia sp.

<400> 41
Met Asp Tyr Val Asn Ile Leu Leu Gly Leu Phe Phe Thr Trp Phe Leu
1 5 10 15
Val Asn Gly Leu Met Ser Leu Arg Arg Arg Lys Ile Ser Lys Lys Leu
20 25 30

Pro Pro Gly Pro Phe Pro Leu Pro Ile Ile Gly Asn Leu His Leu Leu
 35 40 45
 Gly Asn His Pro His Lys Ser Leu Ala Gln Leu Ala Lys Ile His Gly
 50 55 60
 Pro Ile Met Asn Leu Lys Leu Gly Gln Leu Asn Thr Val Val Ile Ser
 65 70 75 80
 Ser Ser Val Val Ala Arg Glu Val Leu Gln Lys Gln Asp Leu Thr Phe
 85 90 95
 Ser Asn Arg Phe Val Pro Asp Val Val His Val Arg Asn His Ser Asp
 100 105 110
 Phe Ser Val Val Trp Leu Pro Val Asn Ser Arg Trp Lys Thr Leu Arg
 115 120 125
 Lys Ile Met Asn Ser Ser Ile Phe Ser Gly Asn Lys Leu Asp Gly Asn
 130 135 140

Gln His Leu Arg Ser Lys Lys Val Gln Glu Leu Ile Asp Tyr Cys Gln
 145 150 155 160
 Lys Cys Ala Lys Asn Gly Glu Ala Val Asp Ile Gly Arg Ala Thr Phe
 165 170 175
 Gly Thr Thr Leu Asn Leu Leu Ser Asn Thr Ile Phe Ser Lys Asp Leu
 180 185 190
 Thr Asn Pro Phe Ser Asp Ser Ala Lys Glu Phe Lys Glu Leu Val Trp
 195 200 205
 Asn Ile Met Val Glu Ala Gly Lys Pro Asn Leu Val Asp Tyr Phe Pro
 210 215 220
 Phe Leu Glu Lys Ile Asp Pro Gln Gly Ile Lys Arg Arg Met Thr Asn
 225 230 235 240
 Asn Phe Thr Lys Phe Leu Gly Leu Ile Ser Gly Leu Ile Asp Asp Arg
 245 250 255
 Leu Lys Glu Arg Asn Leu Arg Asp Asn Ala Asn Ile Asp Val Leu Asp
 260 265 270
 Ala Leu Leu Asn Ile Ser Gln Glu Asn Pro Glu Glu Ile Asp Arg Asn
 275 280 285
 Gln Ile Glu Gln Leu Cys Leu Asp Leu Phe Ala Ala Gly Thr Asp Thr
 290 295 300
 Thr Ser Asn Thr Leu Glu Trp Ala Met Ala Glu Leu Leu Gln Asn Pro
 305 310 315 320
 His Thr Leu Gln Lys Ala Gln Glu Glu Leu Ala Gln Val Ile Gly Lys
 325 330 335
 Gly Lys Gln Val Glu Glu Ala Asp Val Gly Arg Leu Pro Tyr Leu Arg
 340 345 350
 Cys Ile Val Lys Glu Thr Leu Arg Ile His Pro Ala Ala Pro Leu Leu
 355 360 365
 Ile Pro Arg Lys Val Glu Glu Asp Val Glu Leu Ser Thr Tyr Ile Ile
 370 375 380
 Pro Lys Asp Ser Gln Val Leu Val Asn Val Trp Ala Ile Gly Arg Asn
 385 390 395 400
 Ser Asp Leu Trp Glu Asn Pro Leu Val Phe Lys Pro Glu Arg Phe Trp
 405 410 415
 Glu Ser Glu Ile Asp Ile Arg Gly Arg Asp Phe Glu Leu Ile Pro Phe
 420 425 430
 Gly Ala Gly Arg Arg Ile Cys Pro Gly Leu Pro Leu Ala Met Arg Met
 435 440 445
 Ile Pro Val Ala Leu Gly Ser Leu Leu Asn Ser Phe Asn Trp Lys Leu
 450 455 460
 Tyr Gly Gly Ile Ala Pro Lys Asp Leu Asp Met Gln Glu Lys Phe Gly
 465 470 475 480
 Ile Thr Leu Ala Lys Ala Gln Pro Leu Leu Ala Ile Pro Thr Pro Leu
 485 490 495

<210> 42
 <211> 513
 <212> PRT
 <213> Arabidopsis thaliana

<400> 42
 Met Ala Thr Leu Phe Leu Thr Ile Leu Leu Ala Thr Val Leu Phe Leu
 1 5 10 15
 Ile Leu Arg Ile Phe Ser His Arg Arg Asn Arg Ser His Asn Asn Arg
 20 25 30
 Leu Pro Pro Gly Pro Asn Pro Trp Pro Ile Ile Gly Asn Leu Pro His
 35 40 45
 Met Gly Thr Lys Pro His Arg Thr Leu Ser Ala Met Val Thr Thr Tyr
 50 55 60
 Gly Pro Ile Leu His Leu Arg Leu Gly Phe Val Asp Val Val Val Ala
 65 70 75 80
 Ala Ser Lys Ser Val Ala Glu Gln Phe Leu Lys Ile His Asp Ala Asn
 85 90 95
 Phe Ala Ser Arg Pro Pro Asn Ser Gly Ala Lys His Met Ala Tyr Asn
 100 105 110
 Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly His Arg Trp Arg Leu Leu
 115 120 125
 Arg Lys Ile Ser Ser Val His Leu Phe Ser Ala Lys Ala Leu Glu Asp
 130 135 140
 Phe Lys His Val Arg Gln Glu Glu Val Gly Thr Leu Thr Arg Glu Leu
 145 150 155 160
 Val Arg Val Gly Thr Lys Pro Val Asn Leu Gly Gln Leu Val Asn Met
 165 170 175
 Cys Val Val Asn Ala Leu Gly Arg Glu Met Ile Gly Arg Arg Leu Phe
 180 185 190
 Gly Ala Asp Ala Asp His Lys Ala Asp Glu Phe Arg Ser Met Val Thr
 195 200 205
 Glu Met Met Ala Leu Ala Gly Val Phe Asn Ile Gly Asp Phe Val Pro
 210 215 220
 Ser Leu Asp Trp Leu Asp Leu Gln Gly Val Ala Gly Lys Met Lys Arg
 225 230 235 240
 Leu His Lys Arg Phe Asp Ala Phe Leu Ser Ser Ile Leu Lys Glu His
 245 250 255
 Glu Met Asn Gly Gln Asp Gln Lys His Thr Asp Met Leu Ser Thr Leu
 260 265 270
 Ile Ser Leu Lys Gly Thr Asp Leu Asp Gly Asp Gly Ser Leu Thr
 275 280 285
 Asp Thr Glu Ile Lys Ala Leu Leu Asn Met Phe Thr Ala Gly Thr
 290 295 300
 Asp Thr Ser Ala Ser Thr Val Asp Trp Ala Ile Ala Glu Leu Ile Arg
 305 310 315 320
 His Pro Asp Ile Met Val Lys Ala Gln Glu Glu Leu Asp Ile Val Val
 325 330 335

Gly Arg Asp Arg Pro Val Asn Glu Ser Asp Ile Ala Gln Leu Pro Tyr
340 345 350

Leu Gln Ala Val Ile Lys Glu Asn Phe Arg Leu His Pro Pro Thr Pro
355 360 365

Leu Ser Leu Pro His Ile Ala Ser Glu Ser Cys Glu Ile Asn Gly Tyr
370 375 380

His Ile Pro Lys Gly Ser Thr Leu Leu Thr Asn Ile Trp Ala Ile Ala
385 390 395 400

Arg Asp Pro Asp Gln Trp Ser Asp Pro Leu Ala Phe Lys Pro Glu Arg
405 410 415

Phe Leu Pro Gly Gly Glu Lys Ser Gly Val Asp Val Lys Gly Ser Asp
420 425 430

Phe Glu Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu
435 440 445

Ser Leu Gly Leu Arg Thr Ile Gln Phe Leu Thr Ala Thr Leu Val Gln
450 455 460

Gly Phe Asp Trp Glu Leu Ala Gly Gly Val Thr Pro Glu Lys Leu Asn
465 470 475 480

Met Glu Glu Ser Tyr Gly Leu Thr Leu Gln Arg Ala Val Pro Leu Val
485 490 495

Val His Pro Lys Pro Arg Leu Ala Pro Asn Val Tyr Gly Leu Gly Ser
500 505 510

Gly

<210> 43
<211> 7
<212> PRT
<213> Arabidopsis thaliana

<400> 43
Arg Pro Pro Asn Ser Gly Ala
1 5

<210> 44
<211> 17
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (8)
<223> Xaa can be any amino acid.

<220>
<221> UNSURE
<222> (10)
<223> Xaa cab be any amino acid.

<220>
<221> UNSURE
<222> (15)
<223> Xaa can be any amino acid.

<400> 44
Arg Pro Pro Asn Ser Gly Ala Xaa His Xaa Ala Tyr Asn Tyr Xaa Asp
1 5 10 15

Leu

<210> 45
<211> 521
<212> PRT
<213> Arabidopsis thaliana

<220>
<221> UNSURE
<222> (8)
<223> Xaa can be any amino acid.

<220>
<221> UNSURE
<222> (10)
<223> Xaa cab be any amino acid.

<220>
<221> UNSURE
<222> (15)
<223> Xaa can be any amino acid.

<220>
<221> UNSURE
<222> (18) .. (517)
<223> Xaa can be any amino acid. Positions 18-517
can be 0-500 amino acids.

<400> 45
Arg Pro Pro Asn Ser Gly Ala Xaa His Xaa Ala Tyr Asn Tyr Xaa Asp
1 5 10 15

Leu Xaa
20 25 30

Xaa
35 40 45

Xaa
50 55 60

Xaa
65 70 75 80

Xaa
85 90 95

Xaa
100 105 110

Xaa
115 120 125

Xaa
 130 135 140

Xaa
 145 150 155 160

Xaa
 165 170 175

Xaa
 180 185 190

Xaa
 195 200 205

Xaa
 210 215 220

Xaa
 225 230 235 240

Xaa
 245 250 255

Xaa
 260 265 270

Xaa
 275 280 285

Xaa
 290 295 300

Xaa
 305 310 315 320

Xaa
 325 330 335

Xaa
 340 345 350

Xaa
 355 360 365

Xaa
 370 375 380

Xaa
 385 390 395 400

Xaa
 405 410 415

Xaa
 420 425 430

Xaa
 435 440 445

Xaa
 450 455 460

Xaa
465 470 475 480

Xaa
485 490 495

Xaa
500 505 510

Xaa Xaa Xaa Xaa Gly Gly Glu Lys
515 520